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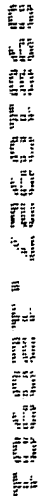
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Map of a First IL-17 Receptor Like cDNA (SEQ ID No: 1)
and Amino Acid (SEQ ID NO: 2)

1 ATAAAAGCGCAGCGTGCGGGTGGCCTGGATCCCGCGCAGTGGCCCGCGATGCTGCTCTCG 60
M S L V -

61 GCTGCTAAGCCTGGCCGCGCTGTGCAGGAGCGCCGTACCCCGAGAGCCGACCGTTCAATG 120
L L S L A A L C R S A V P R E P T V Q C -

121 TGGCTCTGAAACTGGGCCATCTCCAGAGTGGATGCTACAACATGATCTAATCCCCGGAGA 180
G S E T G P S P E W M L Q H D L I P G D -

181 CTTGAGGGACCTCCGAGTAGAACCTGTTACAACACTAGTGTGCAACAGGGGACTATTCAAT 240
L R D L R V E P V T T S V A T G D Y S I -

241 TTTGATGAATGTAAGCTGGGTACTCCGGGCAGATGCCAGCATCCGCTTGTGTAAGGCCAC 300
L M N V S W V L R A D A S I R L L K A T -

301 CAAGATTTGTGTGACGGGCAAAAGCAACTTCCAGTCCTACAGCTGTGTGAGGTGCAATTA 360
K I C V T G K S N F Q S Y S C V R C N Y -

361 CACAGAGGCCTTCCAGACTCAGACCAGACCCTCTGGTGGTAAATGGACATTTTCCTACAT 420
T E A F Q T Q T R P S G G K W T F S Y I -

421 CGGCTTCCTGTAGAGCTGAACACAGTCTATTTTCATTGGGGCCCATAATATTCCTAATGC 480
G F P V E L N T V Y F I G A H N I P N A -

481 AAATATGAATGAAGATGGCCCTTCCATGTCTGTGAATTTACCTCACCAGGCTGCCTAGA 540
N M N E D G P S M S V N F T S P G C L D -

541 CCACATAATGAAATATAAAAAAAGTGTGTCAAGGCCGGAAGCCTGTGGGATCCGAACAT 600
H I M K Y K K K C V K A G S L W D P N I -

601 CACTGCTTGTAAGAAGAATGAGGAGACAGTAGAAGTGAAGTTCACAACCACTCCCCTGGG 660
T A C K K N E E T V E V N F T T T P L G -

661 AAACAGATACATGGCTCTTATCCAACACAGCACTATCATCGGGTTTTCTCAGGTGTTTGA 720
N R Y M A L I Q H S T I I G F S Q V F E -

721 GCCACACCAGAAGAAACAAACGCGAGCTTCAGTGGTGATTCCAGTGACTGGGGATAGTGA 780
P H Q K K Q T R A S V V I P V T G D S E -

781 AGGTGCTACGGTGCAGCTGACTCCATATTTTCTACTTGTGGCAGCGACTGCATCCGACA 840
G A T V Q L T P Y F P T C G S D C I R H -

841 TAAAGGAACAGTTGTGCTCTGCCCACAAACAGGCGTCCCTTTCCCTCTGGATAACAACAA 900
K G T V V L C P Q T G V P F P L D N N K -

901 AAGCAAGCCGGGAGGCTGGCTGCCTCTCCTCCTGCTGTCTCTGCTGGTGGCCACATGGGT 960
S K P G G W L P L L L L S L L V A T W V -

[illegible]

FIGURE 2
Homology of a First IL-17 human Receptor Like Polypeptide
Amino Acid Sequence (SEQ ID NO: 2) and Known Human IL-17
Receptor Family Member (SEQ ID NO: 3)

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1 .....MSLVLLSLAALCRSAVPREP 20
                                     || || || |
1 MGAARSPPSAVPGPLLGLLLLLLGV LAPGGASLRLLDHRALVCSQPGLNC 50
21 TVQCGSETGPSPEWMLQHDLPDGLRDLRVEPVTTTSVATGDYSILMNVS 70
   || . . | . . | . . | . . | . . | . . | . . | . . |
51 TVK..NSTCLDDSWIHPRNLTPSSPKDLQIQLFHAHTQQGDLPVVAHIEW 98
71 VLRADASIRLLKATKICVTGKSNFQSYSCVRCNYTEAFQTQTRPSGGKWT 120
   | . |||| | . . : | . | ||| . . | . . | . . |
99 TLQTDASILYLEGAELSVLQLNTNERLCVRFE....FLSKLRHHHRRWR 143
121 FSYIGFPVELNTVYFIGAHNIPNANMNEDGPSMSVNFTSPGCLDHIMKYK 170
   | . : | : . | : | . : | . | || | . . | . . |
144 FTFSHFVDPDQYEYEVTVHHLPKPIPDGDPNHQSKNFLVPDCEHARMKVT 193
171 KKC VKAGSLWDPNITACKKNEETVEVNFTTTPLGNRYMALI.....QH 213
   | . . ||||| | . . | . | | : | . . | . . |
194 TPCMSSGSLWDPNITVETLEAHQLRVSTLWNESTHYQILLTSFPHMENH 243
214 STIIGFSQVFEPHQKQTRASVVIPVTGDSEGA...TVQLTPYFPTCGSD 260
   | : | : | . . . | | . . | . . | : | : | . . |
244 SCFEHMHHIPAPRPEEFHQRSNVTLTLRNLKGCCRHHQVQIQPFSSCLND 293
261 CIRHKGTVVLCPO.TGVPFPLDNNKSKPGGWLPLLLLSLLVATWVLVAGI 309
   | : || | | || : | : . | : : | : | . . | . . |
294 CLRHSAT.VSCPEMPDTPPEIPDYMPLWVYWF.ITGISILLVGSVILLIV 341
310 YLMWRHERIKKTSFSTTT.....LLP....PIKVLVVYPSE.ICF 344
   : || : | : | : | : | : | : | : | : | : | : |
342 CMTWRLAGPGSEKYSDDTKYTDGLPAADLIPPPLKPRKWIIYSADHPLY 391
345 HHTICYFTEFLQNHCRSEVILEKWQKKKIAEMGPVQWLATQK....KAAD 390
   : | : || | . || | : : . | . | . | . | . | . |
392 VDVVLKFAQFLLTACGTEVALDLLEEQAISEAGVMTWVGRQKQEMVESNS 441
391 KVVFLLSNDVNSVCDGTCGKSEGPS.....SENSQDLFPLAFNLCSD 433
   | : | | . . . | : | . | . | . | . | . | . |
442 KIIVLCSRGTRAKWQALLGR..GAPVRLRCDHGKPVGDLFTAAMNMILPD 489
434 LRSQIHLHKYVVVYFREIDTKDDY.NALSVCPKYHLMK..DATAFCAELL 480
   : ||| || | : | . | : | . | : | . | : |
490 FKRPACFGTYVVCYFSEVSCDGDVPDLFGAAPRYPLMDRFEEVYFRIQDL 539
481 HVKQQVSAGKRSQACHDGCCSL*..... 503
   . | : : |
540 EMFQPGRMHRVGELSGDNYLRSPGGRQLRAALDRFRDWQVRCPDWFECE 589

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FIGURE 3A
Map of a Second Human IL-17 Receptor Like cDNA (SEQ ID NO: 4)
And Amino Acid (SEQ ID NO: 5) Sequences

1 ATAAAAGCGC AGCGTGCGGGTG GCCTGGATCCCG CGCAGTGGCCCG GCGATGTCGCTC GT 60
M S L V -

61 GCTGCTAAG CCTGGCCGCGCT GTGCAGGAGCGC CGTACCCCGAGA GCCGACCGTTCA ATG 120
L L S L A A L C R S A V P R E P T V Q C -

121 TGGCTCTGA AACTGGGCCATC TCCAGAGTGGAT GCTACAACATGA TCTAATCCCCGG AGA 180
G S E T G P S P E W M L Q H D L I P G D -

181 CTTGAGGGA CCTCCGAGTAGA ACCTGTTACAAC TAGTGTGCAAC AGGGGACTATTC AAT 240
L R D L R V E P V T T S V A T G D Y S I -

241 TTTGATGAA TGTAAGCTGGGT ACTCCGGGCAGA TGCCAGCATCCG CTTGTTGAAGGC CAC 300
L M N V S W V L R A D A S I R L L K A T -

301 CAAGATTTG TGTGACGGGCAA AAGCAACTTCCA GTCCTACAGCTG TGTGAGGCTGGAGTG 360
K I C V T G K S N F Q S Y S C V R L E C -

361 CAGTGGTGC GATCATGGCTCG CTGCGACCTCAA TCTTCTGGGCTC AAGCGATCGTTC TGC 420
S G A I M A R C D L N L L G S S D R S A -

421 TTCAGCCTC CCGAGCGGCTGG GACTGCAGGCGT GGGCCACCAGAC CTGGCTAATTTT TGT 480
S A S R A A G T A G V G H Q T W L I F V -

481 AGTTTTTGT AGAGGGGGGTTT CACCGTGTGCT GGTCTTGAATTC CAGTGCTCAGGC GAT 540
V F V E G G F T V L L V L N S S A Q A I -

541 CTGCCTGCC TCGGCTTCCCAA AGTGCTGGGATT ACAGTGGACATT TTCCTACATCGG CTT 600
C L P R L P K V L G L Q W T F S Y I G F -

601 CCCTGTAGA GCTGAACACAGT CTATTTTATTGG GGCCCATATAT TCCTAATGCAAA TAT 660
P V E L N T V Y F I G A H N I P N A N M -

661 GAATGAAGA TGGCCCTTCCAT GTCTGTGAATTT CACCTCACCAGG CTGCCTAGACCA CAT 720
N E D G P S M S V N F T S P G C L D H I -

721 AATGAAATA TAAAAAAAAGTG TGTCAAGGCCGG AAGCCTGTGGGA TCCGAACATCAC TGC 780
M K Y K K K C V K A G S L W D P N I T A -

781 TTGTAAGAA GAATGAGGAGAC AGTAGAAGTGAA CTTACAACCAC TCCCCTGGGAAA CAG 840
C K K N E E T V E V N F T T T P L G N R -

841 ATACATGGC TCTTATCCAACA CAGCACTATCAT CGGGTTTTCTCA GGTGTTTGGCC ACA 900
Y M A L I Q H S T I I G F S Q V F E P H -

901 CCAGAAGAA ACAAACGCGAGC TTCAGTGGTGAT TCCAGTGA CTGG GGATAGTGAAGG TGC 960
Q K K Q T R A S V V I P V T G D S E G A -

961 TACGGTGCA GCTGACTCCATA TTTTCTACTTGG TGGCAGCGACTG CATCCGACATAA AGG 1020
T V Q L T P Y F P T C G S D C I R H K G -

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Figure 3B

1021 AACAGTTGT GCTCTGCCCACA AACAGGCGTCCC TTTCCCTCTGGA TAACAACAAAAG CAA 1080
T V V L C P Q T G V P F P L D N N K S K -

1081 GCCGGGAGG CTGGCTGCCTCT CCTCCTGCTGTC TCTGCTGGTGGC CACATGGGTGCT GGT 1140
P G G W L P L L L L S L L V A T W V L V -

1141 GGCAGGGAT CTATCTAATGTG GAGGCACGAAAG GATCAAGAAGAC TTCCTTTTCTAC CAC 1200
A G I Y L M W R H E R I K K T S F S T T -

1201 CACACTACT GGGGGGCATTAA GGTCTTGTGGT TTACCCATCTGA AATATGTTTCCA TCA 1260
T L L P P I K V L V V Y P S E I C F H H -

1261 CACAATTTG TTACTTCACTGA ATTTCTTCAAAA CCATTGCAGAAG TGAGGTCATCCT CGA 1320
T I C Y F T E F L Q N H C R S E V I L E -

1321 AAAGTGGA GAAAAAGAAAAT AGCAGAGATGGG TCCAGTGCAGTG GCTTGCCACTCA AAA 1380
K W Q K K K I A E M G P V Q W L A T Q K -

1381 GAAGGCAGC AGACAAAGTCGT CTCCTTCTTTC CAATGACGTCAA CAGTGTGTGCGA TGG 1440
K A A D K V V F L L S N D V N S V C D G -

1441 TACCTGTGG CAAGAGCGAGGG CAGTCCCAGTGA GAACTCTCAAGA CCTCTTCCCCCT TGC 1500
T C G K S E G S P S E N S Q D L F P L A -

1501 CTTTAACCT TTTCTGCAGTGA TCTAAGAAGCCA GATTCATCTGCA CAAATACGTGGT GGT 1560
F N L F C S D L R S Q I H L H K Y V V V -

1561 CTACTTTAG AGAGATTGATAC AAAAGACGATTA CAATGCTCTCAG TGTCTGCCCCAA GTA 1620
Y F R E I D T K D D Y N A L S V C P K Y -

1621 CCACCTCAT GAAGGATGCCAC TGCTTTCTGTGC AGAACTTCTCCA TGTCAAGCAGCA GGT 1680
H L M K D A T A F C A E L L H V K Q Q V -

1681 GTCAGCAGG AAAAAGATCACA AGCCTGCCACGA TGGCTGCTGCTC CTTGTAGCCCCA CCA 1740
S A G K R S Q A C H D G C C S L *

1741 TGAGAAGCA AGAGACCTTAAA GGCTTCCTATCC CACCAATTACAG GGAAAAAACGTG TGA 1800

1801 TGATCCTGA AGCTTACTATGC AGCCTACAAACA GCCTTAGTAATT AAAACATTTTAT ACC 1860

1861 AATAAAATT TTCAAATATTGC TAACTAATGTAG CATTAACTAACG ATTGGAACTAC ATT 1920

1921 TACAACTTC AAAGCTGTTTTA TACATAGAAATC AATTACAGCTTT AATTGAAACTG TAA 1980

1981 CCATTTTGA TAATGCAACAAT AAAGCATCTTCAGC 2015

Sequence

FIGURE 4
Homology of a Second IL-17 Human Receptor Like Polypeptide
Amino Acid Sequence (SEQ ID No: 5) and KNown Human IL 17
Receptor Family Mamber (SEQ ID NO: 3)

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1 MSLVLLSLAALCRSAVPREPTVQCGSETGPSPEWMLQHDLPDGLRDLRV 50
1 .....MGAARS 6
51 EPVTTSVATGDYSILMNVSWVLR.ADASIRLL.KATKICVTGKSNFQSYS 98
7 PP..SAVPGPLLGLLLLLLGLVLPAGGASLRLLDHRALVCSQPGLNCTVKN 54
99 CVRLECSGAIMARCDLNLGSSDRSA.....SASRAAGTAGVGHQNWLI 142
55 STCLDDSW.IHPR...NLTPSSPKDLQIQLHFAHTQQGDLPVAHIEWTL 100
143 ....FVVFVEGGFTVLLVLNSSAQAICL..PRLPKVL..GLQWTFYSYIGF 184
101 QTDASILYLEGAELSVLQLNTN.ERLCVRFEFLSKLRHHHRRWRFTFSHF 149
185 PVELNTVYFIGAHNIPNANMNEDGPSMSVNFTSPGCLDHIMKYKKKCVKA 234
150 VVDPDQYEYEVTVHHLPKPIPDGDPNHQSKNFLVPDCEHARMKVTTPCMSS 199
235 GSLWDPNITACKKNEETVEVNFTTTPLGNRYMALI.....QHSTIIGF 277
200 GSLWDPNITVETLEAHQLRVSFTLWNESTHYQILLTSFPHMENHSCFEHM 249
278 SQVFEPHQKKQTRASVVIPVTGDSEGA...TVQLTPYFPTCGSDCIRHKG 324
250 HHI PAPRPEEFHQRSNVTLTLRNLKGCCRQVQIQPFSSCLNDCLRHS 299
325 TVVLC PQ.TGVFPPLDNNKSKPGGWLPLLLLSLLVATWVLVAGIYLMWRH 373
300 T.VSCPEMPDTPEPIPDYMLWVYWF.ITGISILLVGSVILLIVCMTWRL 347
374 ERIKTSFSTTT.....LLP....PIKVLVVYPSE.ICFHHTICY 408
348 AGPGSEKYSDDTKYTDGLPAADLIPPLKPRKVWIIYSADHPLYVDVVLK 397
409 FTEFLQNHCRSEVILEKWQKKKIAEMGPVQWLATQK...KAADKVVFLL 454
398 FAQFLLTACGTEVALDLLEEQAISEAGVMTWVGRQKQEMVESNSKIIVLC 447
455 SNDVNSVCDGTCGKSEGSP.....SENSQDLFPLAFNLFCSDLRSQIH 497
448 SRGTRAKWQALLGR..GAPVRLRCDHGKPVGDLFTAAMNMILPDFKRPAC 495
498 LHKYVVVYFREIDTKDDY.NALSVCPKYHLMK..DATAFCAELLHVKKQV 544
496 FGTYVVCYFSEVSCDGDVPDLFGAAPRYPLMDRFEEVYFRIQDLEMFPQPG 545
545 SAGKRSQACHDGCCSL*..... 561
546 RMHRVGELSGDNYLRSPPGGRQLRAALDRFRDWQVRCPDWFECENLYSADD 595

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FIGURE 5A
Map of a Third IL-17 Receptor Like cDNA (SEQ ID NO: 6)
and Amino Acid (SEQ ID NO: 7) Sequence

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1 ATAAAAGCGCAGCGTGC GGGTGGCCTGGATCCCGCGCAGTGGCCCGGCGATGTCGCTCGT 60
61 GCTGCTAAGCCTGGCCGCGCTGTGCAGGAGCGCCGTACCCCGAGAGCCGACCGTTCAATG 120
121 TGGCTCTGAAACTGGGCCATCTCCAGAGTGGATGCTACAACATGATCTAATCCCGGGAGA 180
181 CTTGAGGGACCTCCGAGTAGAACCTGTTACAACACTAGTGTTGCAACAGGGGACTATTCAAT 240
241 TTTGATGAATGTAAGCTGGGTACTCCGGGCAGATGTGGACATTTTCCTACATCGGCTTCC 300
      M W T F S Y I G F P -
301 CTGTAGAGCTGAACACAGTCTATTTTCATTGGGGCCCATAATATTCCTAATGCAAATATGA 360
      V E L N T V Y F I G A H N I P N A N M N -
361 ATGAAGATGGCCCTTCCATGTCTGTGAATTTACCTCACCAGGCTGCCTAGACCACATAA 420
      E D G P S M S V N F T S P G C L D H I M -
421 TGAAATATAAAAAAAAAAGTGTGTCAAGGCCGAAGCCTGTGGGATCCGAACATCACTGCTT 480
      K Y K K K C V K A G S L W D P N I T A C -
481 GTAAGAAGAAATGAGGAGACAGTAGAAGTGAAGTTCACAACCACTCCCCTGGGAAACAGAT 540
      K K N E E T V E V N F T T T P L G N R Y -
541 ACATGGCTCTTATCCAACACAGCACTATCATCGGGTTTTCTCAGGTGTTTGAGCCACACC 600
      M A L I Q H S T I I G F S Q V F E P H Q -
601 AGAAGAAACAAACGCGAGCTTCAGTGGTGATTCCAGTGACTGGGGATAGTGAAGGTGCTA 660
      K K Q T R A S V V I P V T G D S E G A T -
661 CGGTGCAGCTGACTCCATATTTTCCTACTTGTGGCAGCGACTGCATCCGACATAAAGGAA 720
      V Q L T P Y F P T C G S D C I R H K G T -
721 CAGTTGTGCTCTGCCCACAAACAGGCGTCCCTTTCCCTCTGGATAACAACAAAAGCAAGC 780
      V V L C P Q T G V P F P L D N N K S K P -
781 CGGGAGGCTGGCTGCCTCTCCTCCTGCTGTCTCTGCTGGTGGCCACATGGGTGCTGGTGG 840
      G G W L P L L L L S L L V A T W V L V A -
841 CAGGGATCTATCTAATGTGGAGGCACGAAAGGATCAAGAAGACTTCCTTTTCTACCACCA 900
      G I Y L M W R H E R I K K T S F S T T T -
901 CACTACTGCCCCCATTAAGGTTCTTGTGGTTTACCCATCTGAAATATGTTTCCATCACA 960
      L L P P I K V L V V Y P S E I C F H H T -
961 CAATTTGTTACTTCACTGAATTTCTTCAAAACCATTGCAGAAGTGAGGTCATCCTCGAAA 1020
      I C Y F T E F L Q N H C R S E V I L E K -
1021 AGTGGCAGAAAAAGAAAAATAGCAGAGATGGGTCCAGTGCAGTGGCTTGCCACTCAAAGA 1080
      W Q K K K I A E M G P V Q W L A T Q K K -
1081 AGGCAGCAGACAAAGTCGTCTTCTTCTTTTCCAATGACGTCAACAGTGTGTGCGATGGTA 1140
      A A D K V V F L L S N D V N S V C D G T -
1141 CCTGTGGCAAGAGCGAGGGCAGTCCCAGTGAGAACTCTCAAGACCTCTTCCCCCTTGCCT 1200
      C G K S E G S P S E N S Q D L F P L A F -

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Figure 5B

1201 TTAACCTTTTCTGCAGTGATCTAAGAAGCCAGATTTCATCTGCACAAATACGTGGTGGTCT 1260
N L F C S D L R S Q I H L H K Y V V V Y -

1261 ACTTTAGAGAGATTGATACAAAAGACGATTACAATGCTCTCAGTGTCTGCCCCAAGTACC 1320
F R E I D T K D D Y N A L S V C P K Y H -

1321 ACCTCATGAAGGATGCCACTGCTTTTCTGTGCAGAACTTCTCCATGTCAAGCAGCAGGTGT 1380
L M K D A T A F C A E L L H V K Q Q V S -

1381 CAGCAGGAAAAAGATCACAAGCCTGCCACGATGGCTGCTGCTCCTTGTAGCCCACCCATG 1440
A G K R S Q A C H D G C C S L *

1441 AGAAGCAAGAGACCTTAAAGGCTTCCTATCCCACCAATTACAGGGAAAAAACGTGTGATG 1500

1501 ATCCTGAAGCTTACTATGCAGCCTACAAACAGCCTTAGTAATTAAAACATTTTATACCAA 1560

1561 TAAAATTTTCAAATATTGCTAACTAATGTAGCATTAACGATTGGAAACTACATTTA 1620

1621 CAACTTCAAAGCTGTTTTATACATAGAAATCAATTACAGCTTTAATTGAAAACGTGAACC 1680

1681 ATTTTGATAATGCAACAATAAAGCATCTTCAGC 1713

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FIGURE 6

Homology of a Third Human IL-17 Receptor Like Polypeptide
Amino Acid Sequence (SEQ ID NO: 7) and Known Human IL-17
Receptor Family Member (SEQ ID NO: 3)

```

1 .....MWTFSYIGFP 10
101 QTDASILYLEGAELSVLQLNTNERLCVRFEFLSKLRHHHRRWRFTFSHFV 150
11 VELNTVYFIGAHNIPNANMNEDGPSMSVNFTSPGCLDHIMKYKKKCVKAG 60
151 VDPDQYEYEVTVHHLPKPIPDGDPNHQSKNFLVPDCEHARMKVTTPCMSSG 200
61 SLWDPNITACKKNEETVEVNFTTTPLGNRYMALI.....QHSTIIGFS 103
201 SLWDPNITVETLEAHQLRVSFTLWNESTHYQILLTSFPHMENHSCFEHMH 250
104 QVFEPHQKKQTRASVVIPVTGDSEGA...TVQLTPYFPTCGSDCIRHKGT 150
251 HIPAPRPEEFHQRSNVTLTLRNLKGCCRHQVQIQPFSSCLNDCLRHSAT 300
151 VVLCPQ.TGVPPFLDNNKSKPGGWLPLLLLSLLVATWVLVAGIYLMWRHE 199
301 .VSCPEMPDTPEPIPDYMWPLWVYWF.ITGISILLVGSVILLIVCMTWRLA 348
200 RIKKTSFSTTT.....LLP....PIKVLVVYPSE.ICFHHTICYF 234
349 GPGSEKYSDDTKYTDGLPAADLIPPLKPRKVWIIYSADHPLYVDVVLKF 398
235 TEFLQNHRSEVILEKWQKKKIAEMGPVQWLATQK....KAADKVVFLLS 280
399 AQFLLTACGTEVALDLLEEQAISEAGVMTWVGRQKQEMVESNSKIIVLCS 448
281 NDVNSVCDGTCGKSEGSP.....SENSQDLFPLAFNLFCSDLRSQIHL 323
449 RGTRAKWQALLGR..GAPVRLRCDHGKPVGDLFTAAMNMILPDFKRPACF 496
324 HKYVVVYFREIDTKDDY.NALSVCPKYHLMK..DATAFCAELLHVKKQVS 370
497 GTYVVCYFSEVSCDGDVPDLFGAAPRYPLMDRFEEVYFRIQDLEMFQPGR 546
371 AGKRSQACHDGCCSL*..... 386
547 MHRVGELSGDNYLRSPGGRQLRAALDRFRDWQVRCPDWFEENLYSADDQ 596

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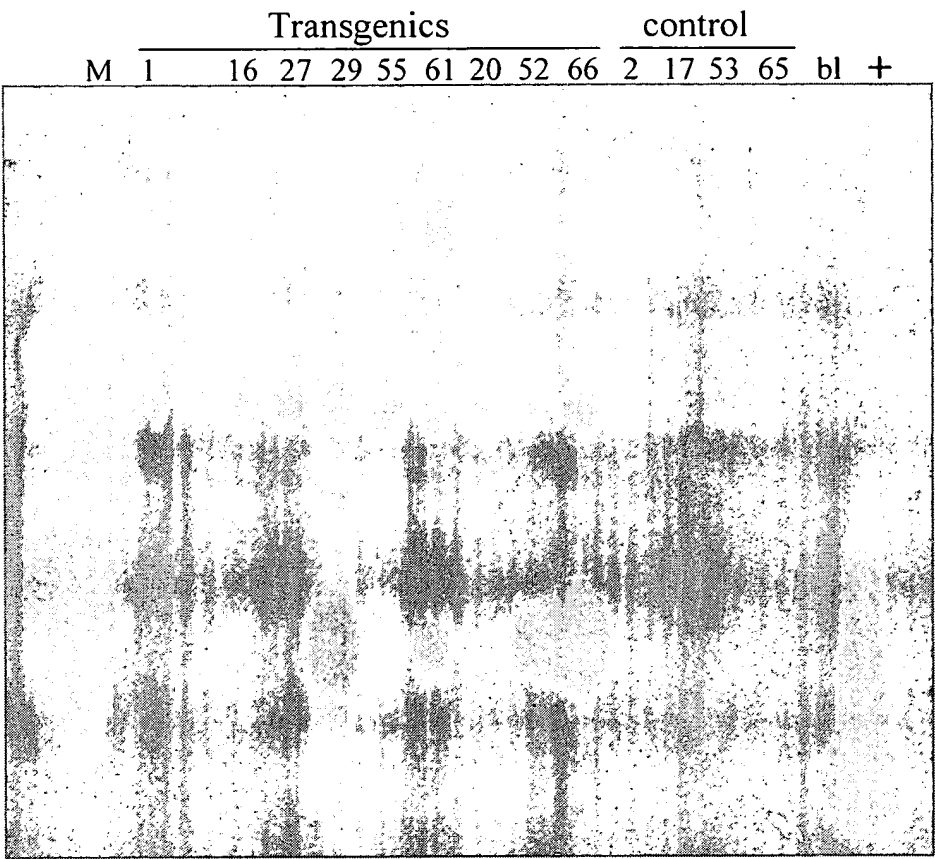
Sequence alignment of the amino acid sequence of the third human IL-17 receptor like polypeptide (SEQ ID NO: 7) with the known human IL-17 receptor family member (SEQ ID NO: 3). The alignment shows high homology between the two sequences, with conserved regions highlighted by vertical bars.

FIGURE 7
Overlap of Amino Acid Sequences of the First (SEQ ID NO: 2),
Second (SEQ ID NO: 5), and Third (SEQ ID NO: 7) Human IL-17
Receptor Like Polypeptides

1	MSLVLLS LAA	LCRS	AVPREP	TVQCGSETG P	SPEWMLQHDL	IPGDLRDLRV
1	MSLVLLS LAA	LCRS	AVPREP	TVQCGSETG P	SPEWMLQHDL	IPGDLRDLRV
51	EPVTTSVATG	DYSILMNVS	W	VL	RADASIRL	LKATKICVTG KSNFQSYSCV
51	EPVTTSVATG	DYSILMNVS	W	VL	RADASIRL	LKATKICVTG KSNFQSYSCV
101	RCNYTEAFQT	QTRPSGGK	--	-----	-----	-----
101	RLECSGAIMA	RCDLNLLGSS		DRSASASRAA	GTAGVGHQNW	LIFVVFVEGG
119	-----	-----	-----	WTF S	YIGFPVELNT	VYFIGAHNIP
151	FTVLLVLNSS	AQAICLPRLP		KVLGLQWTF S	YIGFPVELNT	VYFIGAHNIP
1				MWTF S	YIGFPVELNT	VYFIGAHNIP
143	NANMNEDGPS	MSVNFTSPGC		LDHIMKYKK K	CVKAGSLWDP	NITACKKNEE
201	NANMNEDGPS	MSVNFTSPGC		LDHIMKYKK K	CVKAGSLWDP	NITACKKNEE
26	NANMNEDGPS	MSVNFTSPGC		LDHIMKYKK K	CVKAGSLWDP	NITACKKNEE
193	TVEVNFT TTP	LGNRYMAL IQ		HSTIIGFSQ V	FEPHQKKQTR	ASVVIPVTGD
251	TVEVNFT TTP	LGNRYMAL IQ		HSTIIGFSQ V	FEPHQKKQTR	ASVVIPVTGD
76	TVEVNFT TTP	LGNRYMAL IQ		HSTIIGFSQ V	FEPHQKKQTR	ASVVIPVTGD
243	SEGATVQ LTP	YFPTCGSD CI		RHKGTVVLC P	QTGVPFPLDN	NKSKPGGWLP
301	SEGATVQ LTP	YFPTCGSD CI		RHKGTVVLC P	QTGVPFPLDN	NKSKPGGWLP
126	SEGATVQ LTP	YFPTCGSD CI		RHKGTVVLC P	QTGVPFPLDN	NKSKPGGWLP
293	<u>LLLLSLL VAT</u>	<u>WVLVAGIYLM</u>		<u>WRHERIKKTS</u>	<u>FSTTTLLPPI</u>	<u>KVLVVYPSEI</u>
351	<u>LLLLSLL VAT</u>	<u>WVLVAGIYLM</u>		<u>WRHERIKKTS</u>	<u>FSTTTLLPPI</u>	<u>KVLVVYPSEI</u>
176	<u>LLLLSLL VAT</u>	<u>WVLVAGIYLM</u>		<u>WRHERIKKTS</u>	<u>FSTTTLLPPI</u>	<u>KVLVVYPSEI</u>
343	CFHHTICYFT	EFLQNHCRSE		VILEKWQKK K	IAEMGPVQWL	ATQKKAADKV
401	CFHHTICYFT	EFLQNHCRSE		VILEKWQKK K	IAEMGPVQWL	ATQKKAADKV
226	CFHHTICYFT	EFLQNHCRSE		VILEKWQKK K	IAEMGPVQWL	ATQKKAADKV
393	VFLLSND VNS	VCDGTCGKSE		GSPSENSQDL	FPLAFNLFCS	DLRSQIHLHK
451	VFLLSND VNS	VCDGTCGKSE		GSPSENSQDL	FPLAFNLFCS	DLRSQIHLHK
276	VFLLSND VNS	VCDGTCGKSE		GSPSENSQDL	FPLAFNLFCS	DLRSQIHLHK
443	YVVVYFREID	TKDDYNAL SV		CPKYHLMKDA	TAFCAELLHV	KQQVSAGKRS
501	YVVVYFREID	TKDDYNAL SV		CPKYHLMKDA	TAFCAELLHV	KQQVSAGKRS
326	YVVVYFREID	TKDDYNAL SV		CPKYHLMKDA	TAFCAELLHV	KQQVSAGKRS
493	QACHDGC CSL	*				
551	QACHDGC CSL	*				
376	QACHDGC CSL	*				

Figure 8

Northern Blot Expression Analysis of TH00-018
Necropsied Transgenic Founders



0.54 kb →

Figure 9

Northern Blot Expression Analysis of TH00-018
Hepatectomized Transgenic Founders

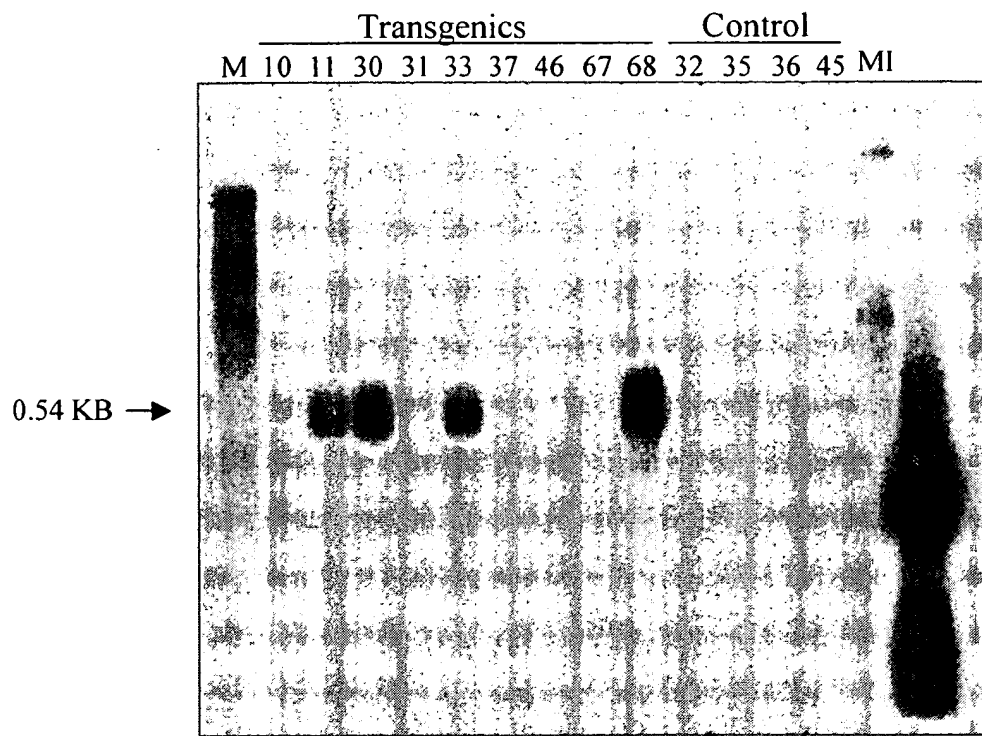


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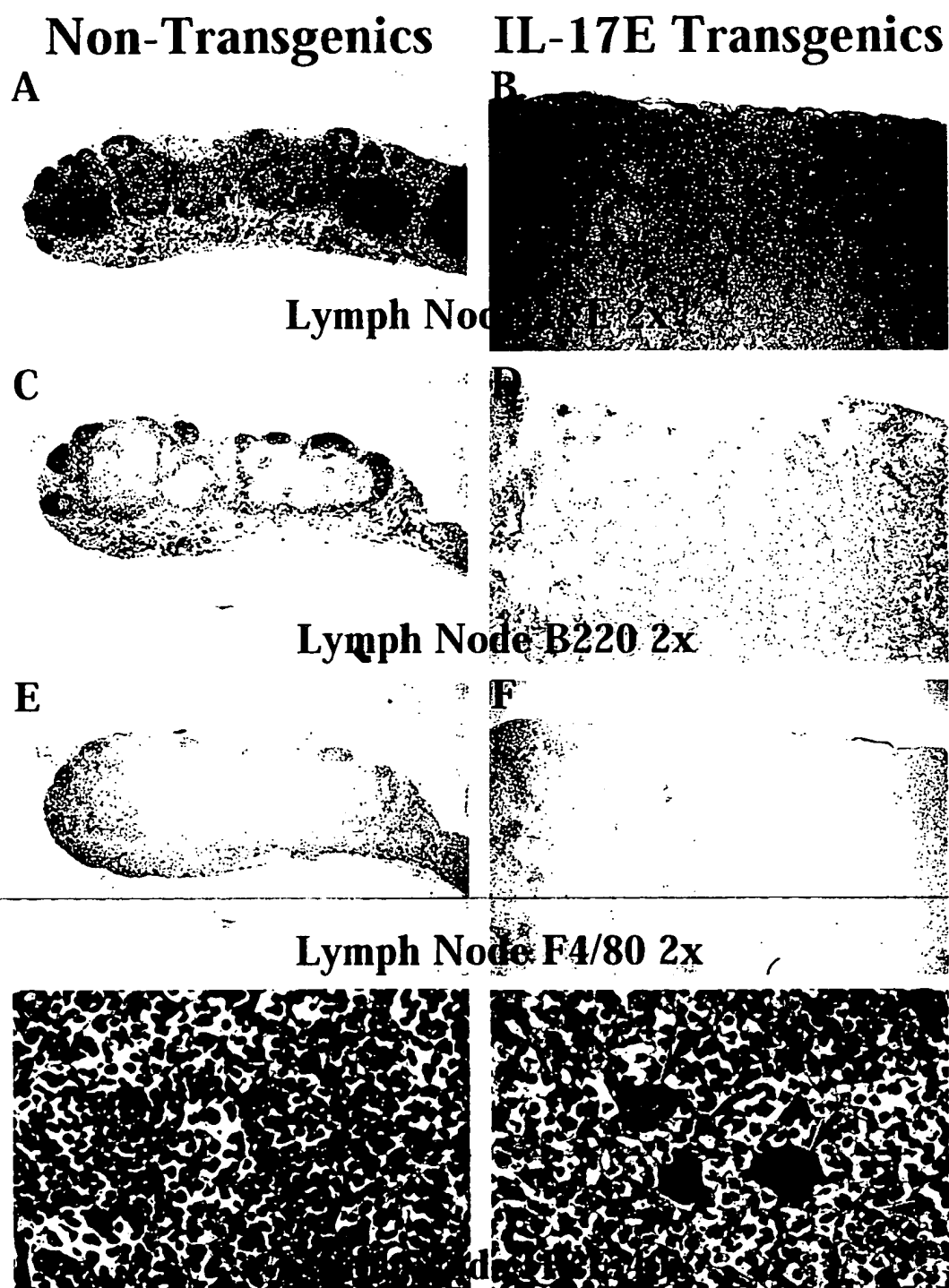


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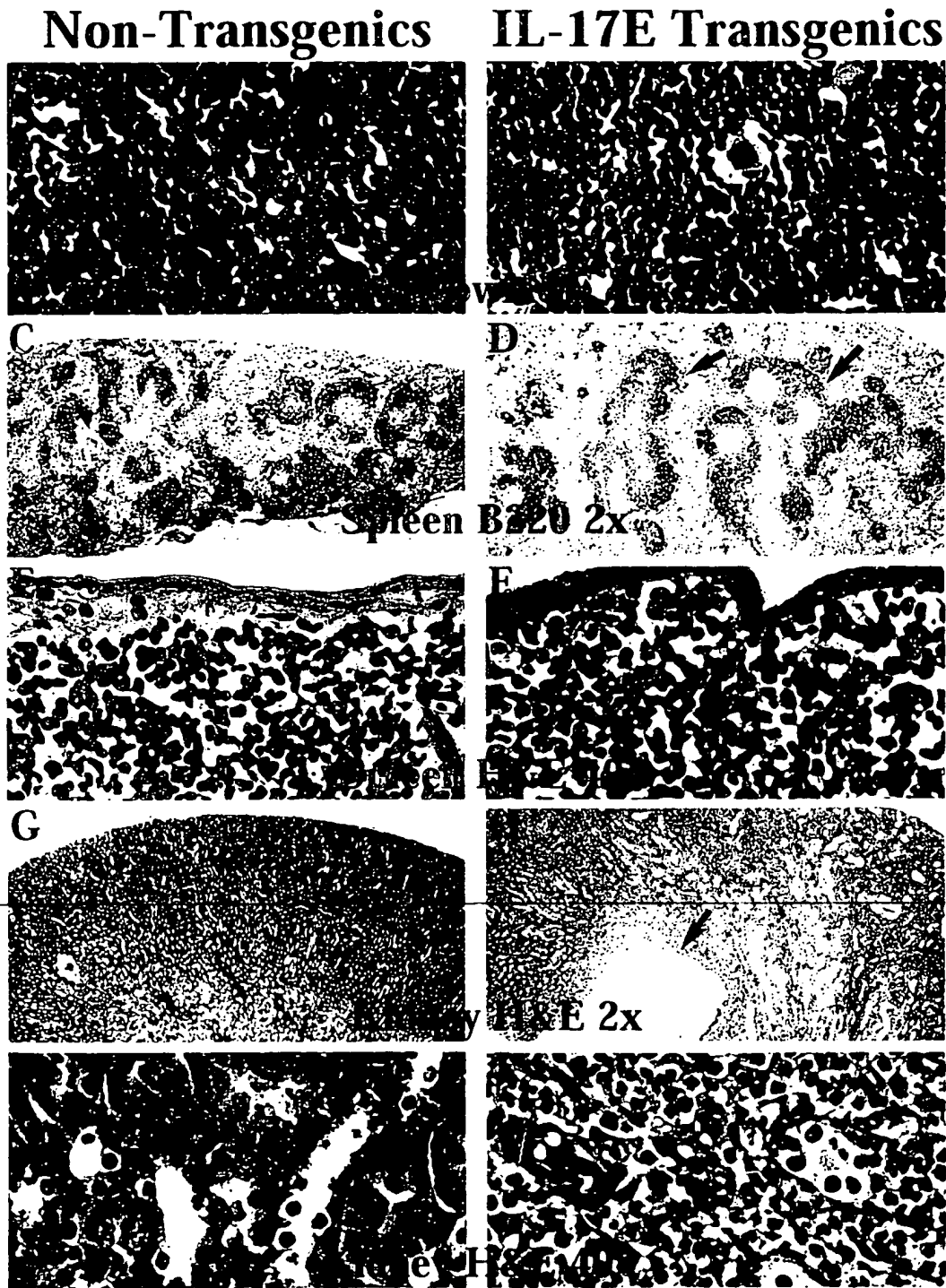


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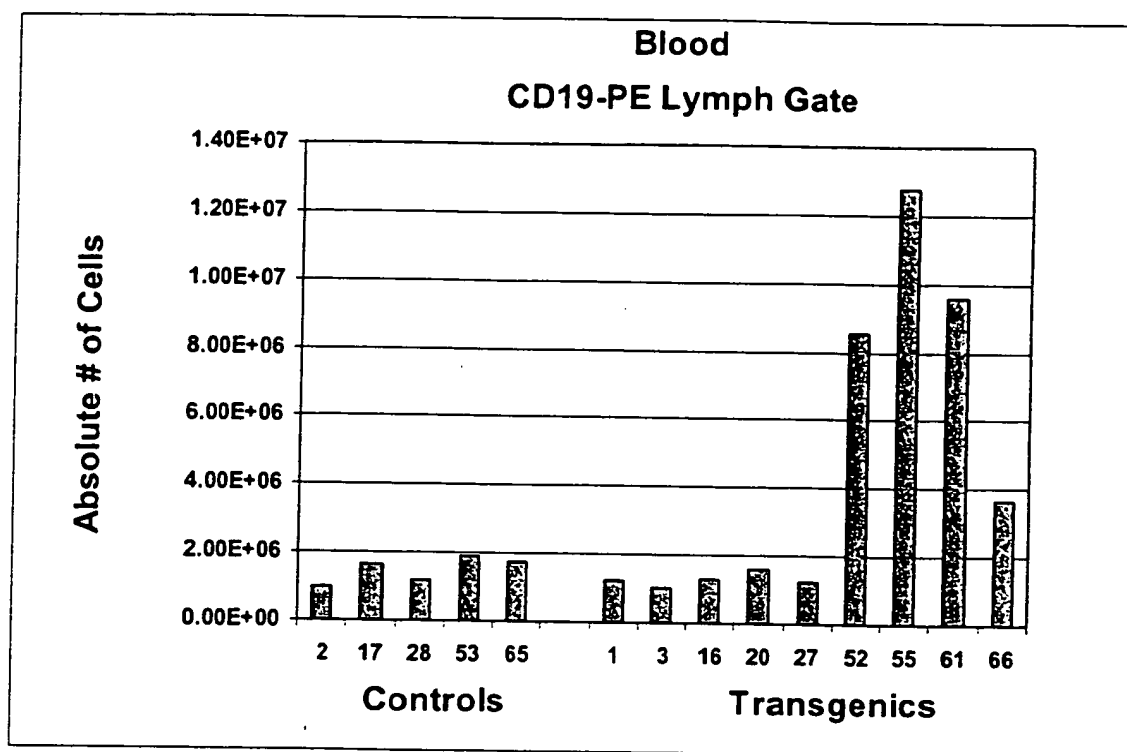


Figure 13

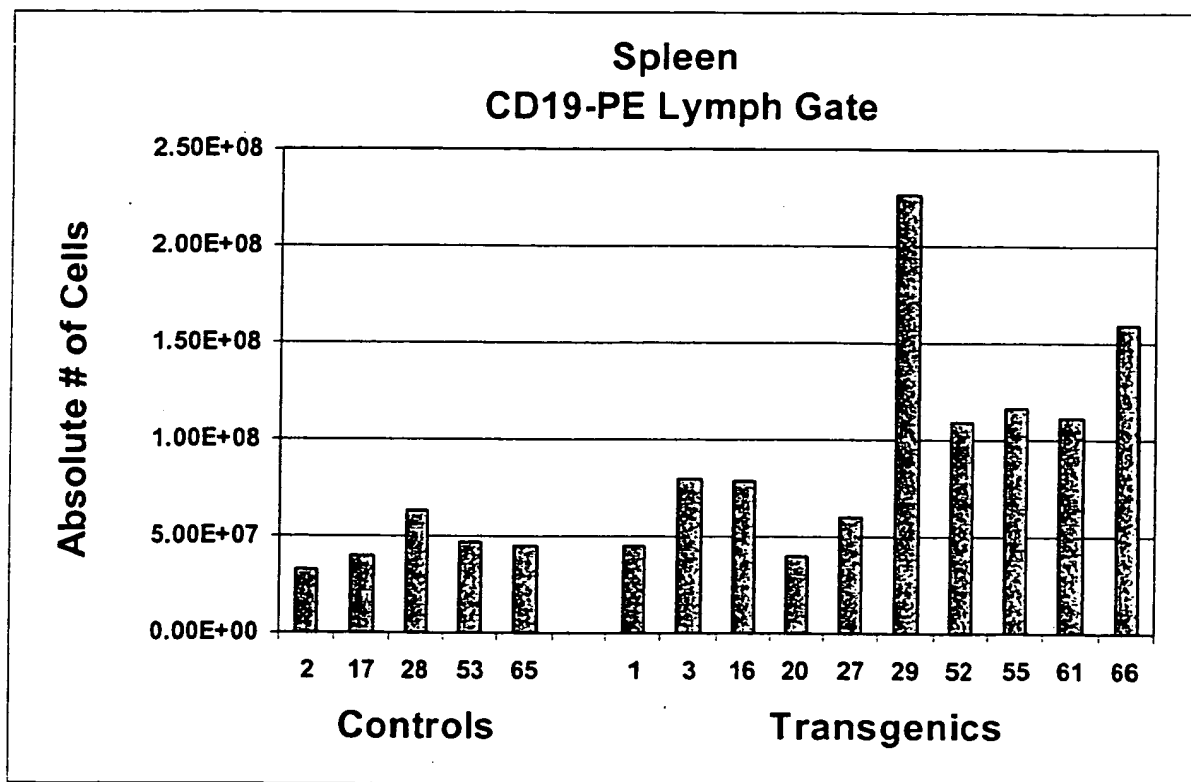


Figure 14

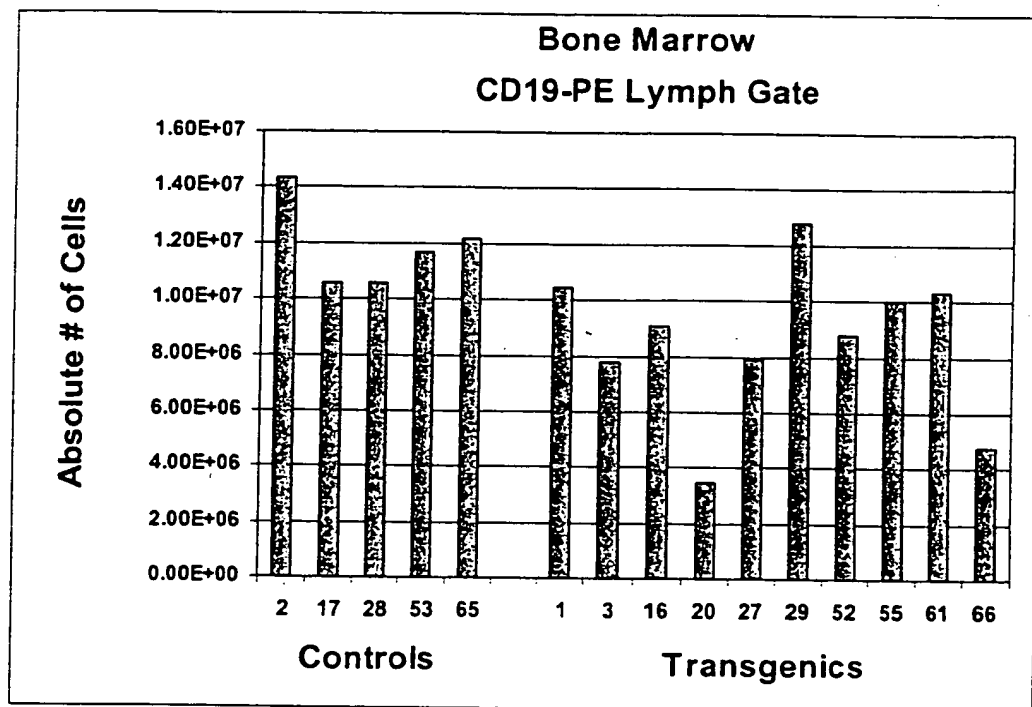


Figure 15

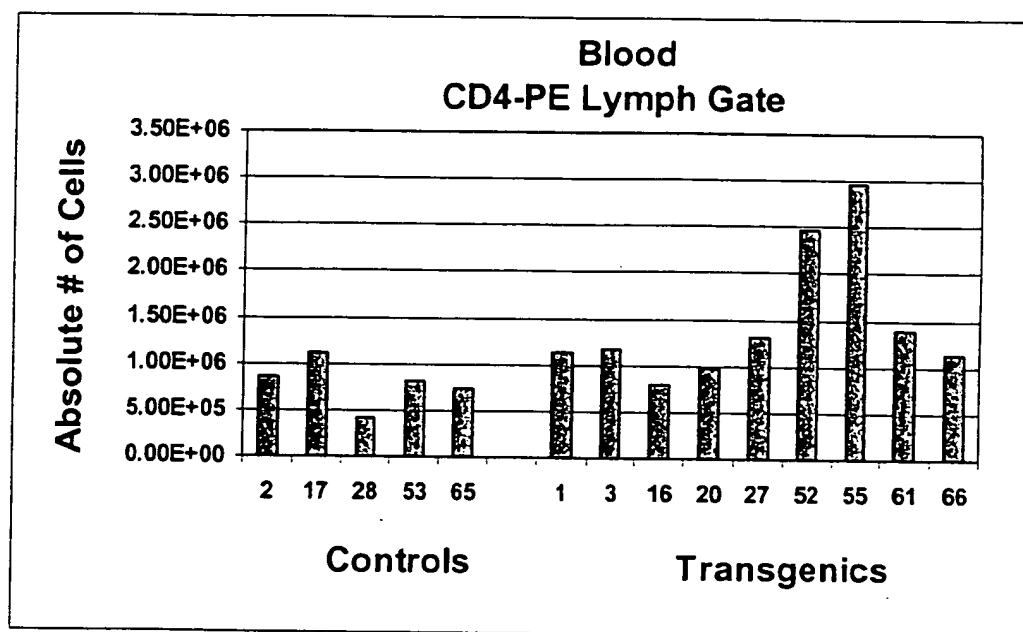


Figure 16

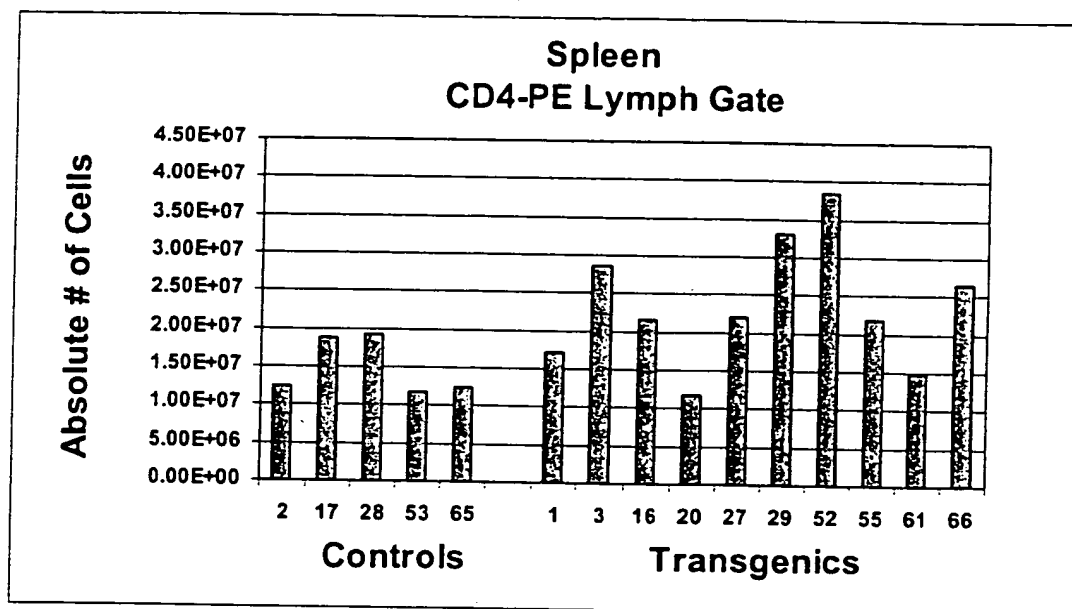


Figure 17

CD45R+ CELLS EXPRESSING IL17Br IN TRANSGENIC BONE MARROW

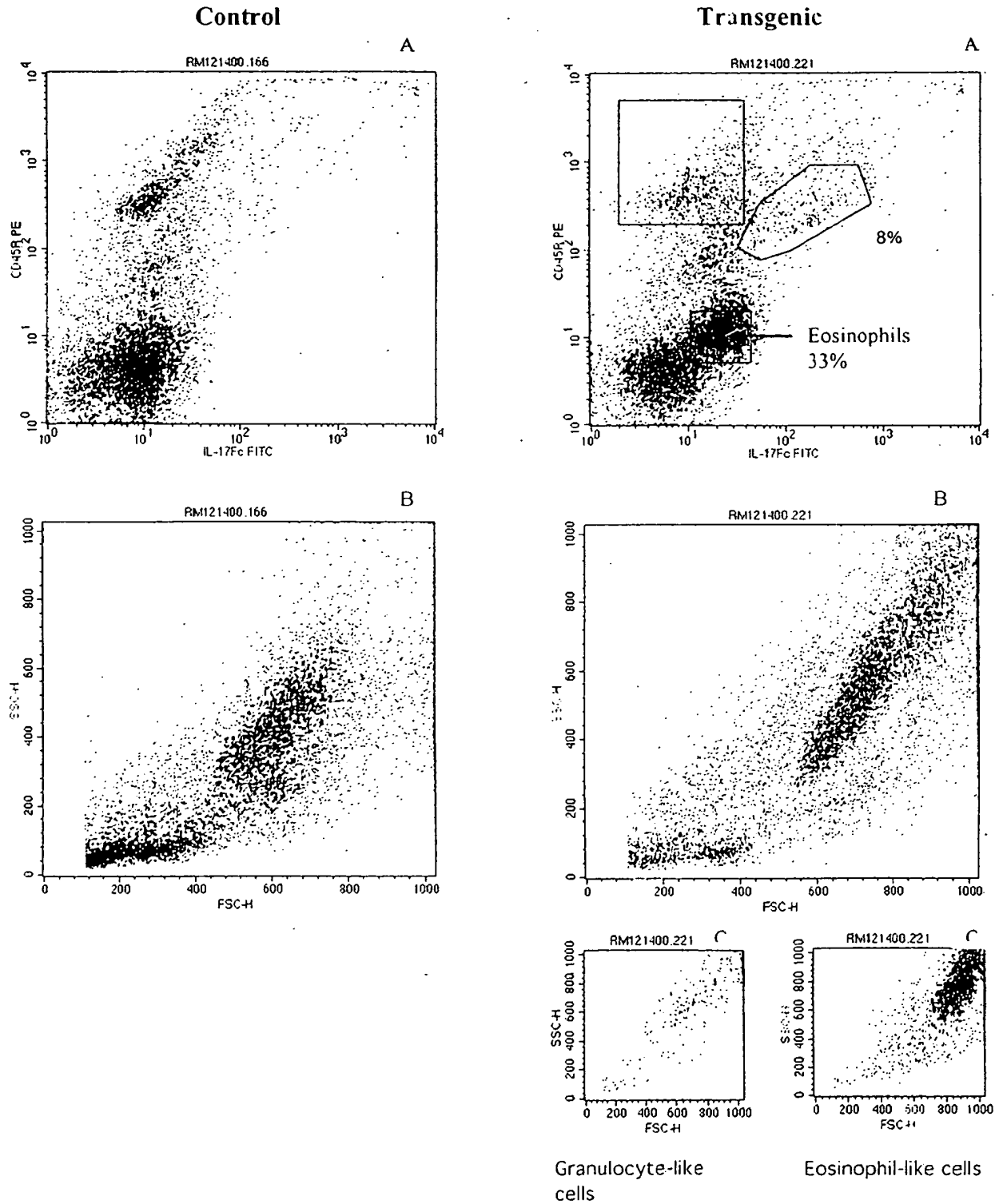
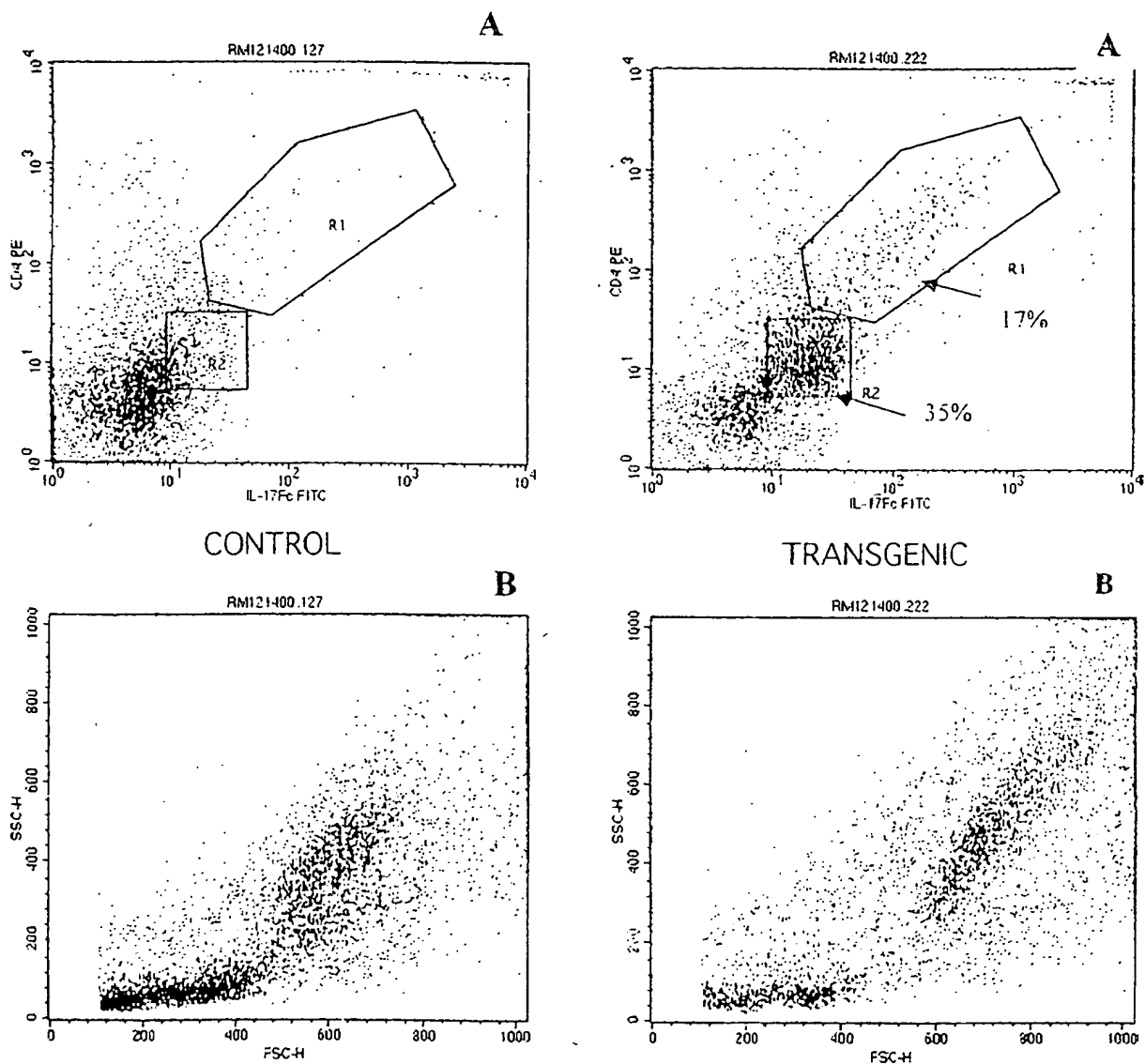


Figure 18

CD4+ CELLS EXPRESSING
IL17Br IN TRANSGENIC BONE
MARROW



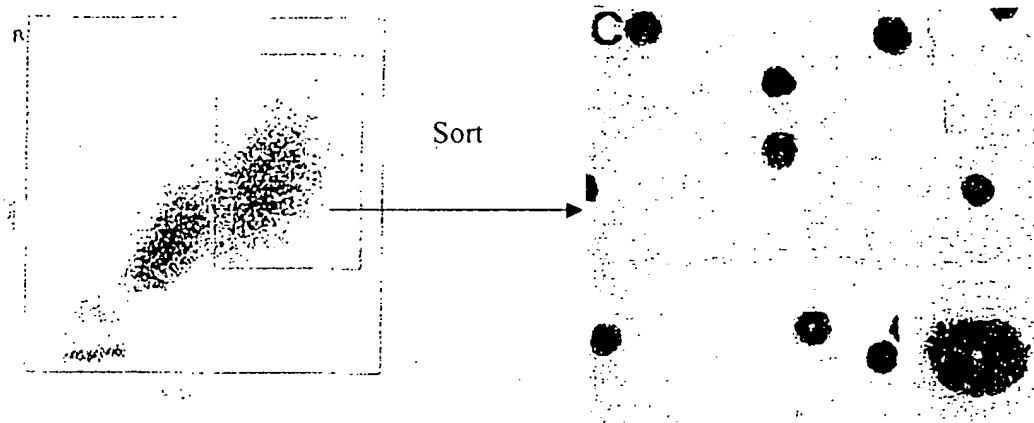
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Figure 19

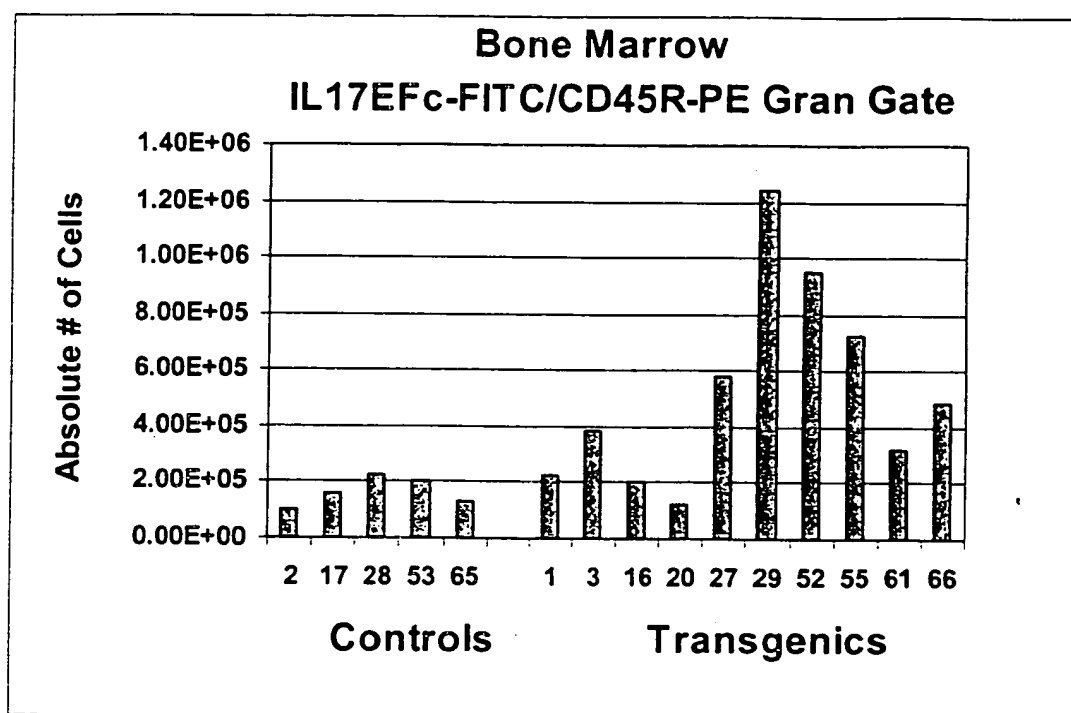
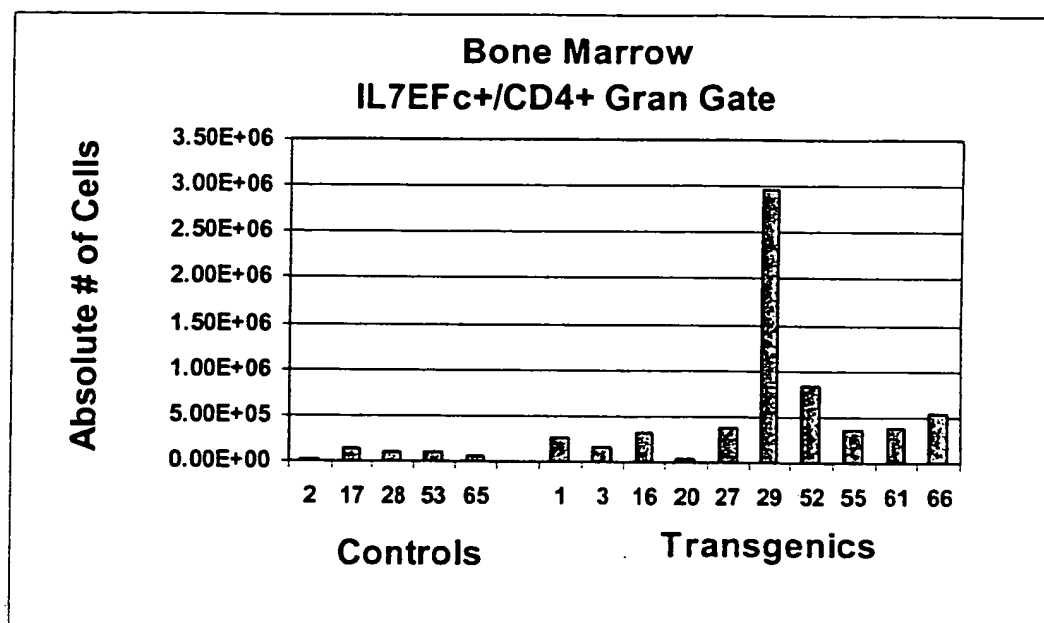


Figure 20



IL-17RB-2 Fusion Protein (SEQ ID NO: 24)

1	<u>MSLVLLSLAA</u>	<u>LCRS</u>	<u>AVPREP</u>	<u>TVQCGSETGP</u>	<u>SPEWMLQHD</u>	<u>LIPGDLRLRV</u>
51	<u>EPVTTSVATG</u>	<u>DYSILMNVSW</u>	<u>VLRADASIRL</u>	<u>LKATKICVTG</u>	<u>KSNFQSYSCV</u>	<u>IPNANMNEDG</u>
101	<u>RCNYTEAFQT</u>	<u>QTRPSGGKWT</u>	<u>FSYIGFPVEL</u>	<u>NTVYFIGAHN</u>	<u>IPNANMNEDG</u>	<u>EETVEVNFTT</u>
151	<u>PSMSVNFTSP</u>	<u>GCLDHIMKYK</u>	<u>KKCVKAGSLW</u>	<u>DPNITACKKN</u>	<u>EETVEVNFTT</u>	<u>GDSEGATVQL</u>
201	<u>TPLGNRYMAL</u>	<u>IQHSTIIGFS</u>	<u>QVFEPHQKKQ</u>	<u>TRASVVIPT</u>	<u>GDSEGATVQL</u>	<u>DNNKSKPGGW</u>
251	<u>TPYFPTCGSD</u>	<u>CIRHKGTVVL</u>	<u>CPQTGVPFPL</u>	<u>DNNKSKPGGW</u>	<u>LPAAAEPKSC</u>	<u>DKTHTCPPCP</u>
301	<u>DKTHTCPPCP</u>	<u>APELLGGPSV</u>	<u>FLFPPKPKDT</u>	<u>LMISRTPEVT</u>	<u>CVVVVDVSHED</u>	<u>PEVKFNWYVD</u>
351	<u>PEVKFNWYVD</u>	<u>GVEVHNAKTK</u>	<u>PREEQYNSTY</u>	<u>RVVSVLTVLH</u>	<u>QDWLNGKEYK</u>	<u>CKVSNKALPA</u>
401	<u>CKVSNKALPA</u>	<u>PIEKTISKAK</u>	<u>GQPREPQVYT</u>	<u>LPPSRDELTK</u>	<u>NQVSLTCLVK</u>	<u>GFYPSDIAVE</u>
451	<u>GFYPSDIAVE</u>	<u>WESNGQPENN</u>	<u>YKTTTPVLDS</u>	<u>DGSFFLYSKL</u>	<u>TVDKSRWQQG</u>	<u>NVFSCSVMHE</u>
501	<u>NVFSCSVMHE</u>	<u>ALHNHYTQKS</u>	<u>LSLSPGK*</u>			

[illegible]

Figure 23

Fusion Protein for IL-17RB-3 (SEQ ID NO: 25)

1 **MSLVLLSLAA** **LCRS**AVPREP TVQCGSETGP SPEWMLQHDL IPGDLRLDRV
51 EPVTTTSVATG DYSILMNVSW VLRADASIRL LKATKICVTG KSNFQSYSCV
101 RLECSGAIMA RCDLNLGSS DRSASASRAA GTAGVGHQTW LIFVVFVEGG
151 FTVLLVLNSS AQAICLPRLP KVLGLQWTFS YIGFPVELNT VYFIGAHNIP
201 NANMNEDGPS MSVNFTSPGC LDHIMKYKKK CVKAGSLWDP NITACKKNEE
251 TVEVNFTTTP LGNRYMALIQ HSTIIGFSQV FEPHQKKQTR ASVVIPVTGD
301 SEGATVQLTP YFPTCGSDCI RHKGTIVLCP QTGVPPFLDN NKSKPGGWLP
351 AAAEPKSCDK THTCPPCPAP ELLGGPSVFL FPPKPKDTLM ISRTPEVTCV
401 VVDVSHEDPE VKFNWYVDGV EVHNATKPR EEQYNSTYRV VSVLTVLHQD
451 WLNGKEYKCK VSNKALPAPI EKTISKAKGQ PREPQVYTLF PSRDELTKNQ
501 VSLTCLVKGF YPSDIAVEWE SNGQPENNYK TTPPVLSDSG SFFLYSKLTV
551 DKSRWQQGNV FSCSVMHEAL HNHYTQKSL LSPGK*